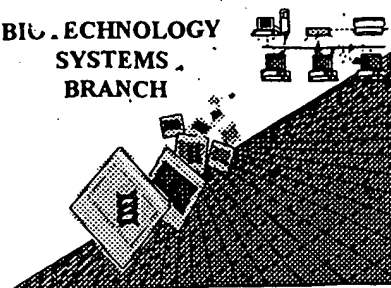# RAW SEQUENCE LISTING
ERROR REPORT

BIO. ECHNOLOGY
SYSTEMS.
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/852,238_

Source: _OIPE_

Date Processed by STIC: _08/17/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/852,238

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

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OIPE

```
          RAW SEQUENCE LISTING            DATE: 08/17/2001
          PATENT APPLICATION:  US/09/852,238     TIME: 11:40:03

          Input Set : A:\51320-AB.txt
          Output Set: N:\CRF3\08162001\I852238.raw

       3 <110> APPLICANT: Graham P. Allaway et al.
       5 <120> TITLE OF INVENTION: USES OF A CHEMOKINE RECEPTOR FOR INHIBITING HIV-1 INFECTION
       7 <130> FILE REFERENCE: 2048/51320-AB/JPW/SHS
       9 <140> CURRENT APPLICATION NUMBER: 09/852,238
C-->  10 <141> CURRENT FILING DATE: 2001-05-09                Does Not Comply
      12 <160> NUMBER OF SEQ ID NOS: 30                 Corrected Diskette Needed
      14 <170> SOFTWARE: PatentIn version 3.0
      16 <210> SEQ ID NO: 1
      17 <211> LENGTH: 38
      18 <212> TYPE: DNA
C-->  19 <213> ORGANISM: artificial
W-->  21 <220> FEATURE:
W-->  21 <223> OTHER INFORMATION:
      21 <400> SEQUENCE: 1
      22 caaggctact tccctgattg gcagaactac acaccagg                          38
      25 <210> SEQ ID NO: 2
      26 <211> LENGTH: 25
      27 <212> TYPE: DNA
C-->  28 <213> ORGANISM: artificial
W-->  30 <220> FEATURE:
W-->  30 <223> OTHER INFORMATION:
      30 <400> SEQUENCE: 2
      31 agcaagccga gtcctgcgtc gagag                                       25
      34 <210> SEQ ID NO: 3
      35 <211> LENGTH: 23
      36 <212> TYPE: DNA
C-->  37 <213> ORGANISM: artificial
W-->  39 <220> FEATURE:
W-->  39 <223> OTHER INFORMATION:
      39 <400> SEQUENCE: 3
      40 gggactttcc gctggggact ttc                                         23
      43 <210> SEQ ID NO: 4
      44 <211> LENGTH: 33
      45 <212> TYPE: DNA
C-->  46 <213> ORGANISM: artificial
W-->  48 <220> FEATURE:
W-->  48 <223> OTHER INFORMATION:
      48 <400> SEQUENCE: 4
      49 cctgttcggg cgccactgct agagattttc cac                              33
      52 <210> SEQ ID NO: 5
      53 <211> LENGTH: 31
      54 <212> TYPE: PRT
      55 <213> ORGANISM: human
      57 <400> SEQUENCE: 5
      59 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
      60 1               5                   10                  15
      62 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg
```

Errored

When field 213 is artificial or unknown, descriptions are required in fields 220 through 223

BEST AVAILABLE COPY

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

```
 63           20                  25                  30
 65 <210> SEQ ID NO: 6
 66 <211> LENGTH: 15
 67 <212> TYPE: PRT
 68 <213> ORGANISM: human
 70 <400> SEQUENCE: 6
 72 His Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln
 73 1               5                  10                  15
 75 <210> SEQ ID NO: 7
 76 <211> LENGTH: 32
 77 <212> TYPE: PRT
 78 <213> ORGANISM: human
 80 <400> SEQUENCE: 7
 82 Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro
 83 1               5                  10                  15
 85 Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val
 86              20                  25                  30
 88 <210> SEQ ID NO: 8
 89 <211> LENGTH: 17
 90 <212> TYPE: PRT
 91 <213> ORGANISM: human
 93 <400> SEQUENCE: 8
 95 Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp
 96 1               5                  10                  15
 98 Gln
101 <210> SEQ ID NO: 9
102 <211> LENGTH: 36
103 <212> TYPE: DNA
C--> 104 <213> ORGANISM: artificial
W--> 106 <220> FEATURE:
W--> 106 <223> OTHER INFORMATION:
106 <400> SEQUENCE: 9
107 aagcttggag aaccagcggt taccatggag gggatc                         36
110 <210> SEQ ID NO: 10
111 <211> LENGTH: 30
112 <212> TYPE: DNA
C--> 113 <213> ORGANISM: artificial
W--> 115 <220> FEATURE:
W--> 115 <223> OTHER INFORMATION:
115 <400> SEQUENCE: 10
116 gtctgagtct gagtcaagct tggagaacca                                30
119 <210> SEQ ID NO: 11
120 <211> LENGTH: 41
121 <212> TYPE: DNA
C--> 122 <213> ORGANISM: artificial
W--> 124 <220> FEATURE:
W--> 124 <223> OTHER INFORMATION:
124 <400> SEQUENCE: 11
125 ctcgagcatc tgtgttagct ggagtgaaaa cttgaagact c                   41
```

RAW SEQUENCE LISTING   DATE: 08/17/2001
PATENT APPLICATION: US/09/852,238   TIME: 11:40:03

Input Set : A:\51320-AB.txt
Output Set: N:\CRF3\08162001\I852238.raw

```
        128 <210> SEQ ID NO: 12
        129 <211> LENGTH: 30
        130 <212> TYPE: DNA
C--> 131 <213> ORGANISM: artificial
W--> 133 <220> FEATURE:
W--> 133 <223> OTHER INFORMATION:
        133 <400> SEQUENCE: 12
        134 gtctgagtct gagtcctcga gcatctgtgt                               30
        137 <210> SEQ ID NO: 13
       .138 <211> LENGTH: 32
        139 <212> TYPE: DNA
C--> 140 <213> ORGANISM: artificial
W--> 142 <220> FEATURE:
W--> 142 <223> OTHER INFORMATION:
        142 <400> SEQUENCE: 13
        143 aagcttcaga gagaagccgg gatggaaact cc                            32
        146 <210> SEQ ID NO: 14
        147 <211> LENGTH: 30
        148 <212> TYPE: DNA
C--> 149 <213> ORGANISM: artificial
W--> 151 <220> FEATURE:
W--> 151 <223> OTHER INFORMATION:
        151 <400> SEQUENCE: 14
        152 gtctgagtct gagtcaagct tcagagagaa                               30
        155 <210> SEQ ID NO: 15
        156 <211> LENGTH: 32
        157 <212> TYPE: DNA
C--> 158 <213> ORGANISM: artificial
W--> 160 <220> FEATURE:
W--> 160 <223> OTHER INFORMATION:
        160 <400> SEQUENCE: 15
        161 ctcgagctga gtcagaaccc agcagagagt tc                            32
        164 <210> SEQ ID NO: 16
        165 <211> LENGTH: 30
        166 <212> TYPE: DNA
C--> 167 <213> ORGANISM: artificial
W--> 169 <220> FEATURE:
W--> 169 <223> OTHER INFORMATION:
        169 <400> SEQUENCE: 16
        170 gtctgagtct gagtcctcga gctgagtcag                               30
        173 <210> SEQ ID NO: 17
        174 <211> LENGTH: 32
        175 <212> TYPE:. DNA
C--> 176 <213> ORGANISM: artificial
W--> 178 <220> FEATURE:
W--> 178 <223> OTHER INFORMATION:
        178 <400> SEQUENCE: 17
        179 aagcttcagt acatccacaa catgctgtcc ac                            32
        182 <210> SEQ ID NO: 18
```

RAW SEQUENCE LISTING   DATE: 08/17/2001
PATENT APPLICATION: US/09/852,238   TIME: 11:40:03

Input Set : A:\51320-AB.txt
Output Set: N:\CRF3\08162001\I852238.raw

```
       183 <211> LENGTH: 30
       184 <212> TYPE: DNA
C--> 185 <213> ORGANISM: artificial
W--> 187 <220> FEATURE:
W--> 187 <223> OTHER INFORMATION:
       187 <400> SEQUENCE: 18
       188 gtctgagtct gagtcaagct tcagtacatc                               30
       191 <210> SEQ ID NO: 19
       192 <211> LENGTH: 31
       193 <212> TYPE: DNA
C--> 194 <213> ORGANISM: artificial
W--> 196 <220> FEATURE:
W--> 196 <223> OTHER INFORMATION:
       196 <400> SEQUENCE: 19
       197 ctcgagcctc gttttataaa ccagccgaga c                             31
       200 <210> SEQ ID NO: 20
       201 <211> LENGTH: 30
       202 <212> TYPE: DNA
C--> 203 <213> ORGANISM: artificial
W--> 205 <220> FEATURE:
W--> 205 <223> OTHER INFORMATION:
       205 <400> SEQUENCE: 20
       206 gtctgagtct gagtcctcga gcctcgtttt                               30
       209 <210> SEQ ID NO: 21
       210 <211> LENGTH: 29
       211 <212> TYPE: DNA
C--> 212 <213> ORGANISM: artificial
W--> 214 <220> FEATURE:
W--> 214 <223> OTHER INFORMATION:
       214 <400> SEQUENCE: 21
       215 aagcttcagg gagaagtgaa atgacaacc                                29
       218 <210> SEQ ID NO: 22
       219 <211> LENGTH: 30
       220 <212> TYPE: DNA
C--> 221 <213> ORGANISM: artificial
W--> 223 <220> FEATURE:
W--> 223 <223> OTHER INFORMATION:
       223 <400> SEQUENCE: 22
       224 gtctgagtct gagtcaagct tcagggagaa                               30
       227 <210> SEQ ID NO: 23
       228 <211> LENGTH: 33
       229 <212> TYPE: DNA
C--> 230 <213> ORGANISM: artificial
W--> 232 <220> FEATURE:
W--> 232 <223> OTHER INFORMATION:
       232 <400> SEQUENCE: 23
       233 ctcgagcaga cctaaaacac aatagagagt tcc                           33
       236 <210> SEQ ID NO: 24
       237 <211> LENGTH: 30
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RAW SEQUENCE LISTING   DATE: 08/17/2001
PATENT APPLICATION: US/09/852,238   TIME: 11:40:03

Input Set : A:\51320-AB.txt
Output Set: N:\CRF3\08162001\I852238.raw

```
       238 <212> TYPE: DNA
C--> 239 <213> ORGANISM: artificial
W--> 241 <220> FEATURE:
W--> 241 <223> OTHER INFORMATION:
       241 <400> SEQUENCE: 24
       242 gtctgagtct gagtcctcga gcagacctaa                        30
       245 <210> SEQ ID NO: 25
       246 <211> LENGTH: 34
       247 <212> TYPE: DNA
C--> 248 <213> ORGANISM: artificial
W--> 250 <220> FEATURE:
W--> 250 <223> OTHER INFORMATION:
       250 <400> SEQUENCE: 25
       251 aagcttctgt agagttaaaa aatgaacccc acgg                   34
       254 <210> SEQ ID NO: 26
       255 <211> LENGTH: 30
       256 <212> TYPE: DNA
C--> 257 <213> ORGANISM: artificial
W--> 259 <220> FEATURE:
W--> 259 <223> OTHER INFORMATION:
       259 <400> SEQUENCE: 26
       260 gtctgagtct gagtcaagct tctgtagagt                        30
       263 <210> SEQ ID NO: 27
       264 <211> LENGTH: 34
       265 <212> TYPE: DNA
C--> 266 <213> ORGANISM: artificial
W--> 268 <220> FEATURE:
W--> 268 <223> OTHER INFORMATION:
       268 <400> SEQUENCE: 27
       269 ctcgagccat ttcatttttc tacaggacag catc                   34
       272 <210> SEQ ID NO: 28
       273 <211> LENGTH: 30
       274 <212> TYPE: DNA
C--> 275 <213> ORGANISM: artificial
W--> 277 <220> FEATURE:
W--> 277 <223> OTHER INFORMATION:
       277 <400> SEQUENCE: 28
       278 gtctgagtct gagtcctcga gccatttcat                        30
       281 <210> SEQ ID NO: 29
       282 <211> LENGTH: 39
       283 <212> TYPE: DNA
C--> 284 <213> ORGANISM: artificial
W--> 286 <220> FEATURE:
W--> 286 <223> OTHER INFORMATION:
       286 <400> SEQUENCE: 29
       287 gtctgagtct gagtcaagct taacaagatg gattatcaa              39
       290 <210> SEQ ID NO: 30
       291 <211> LENGTH: 39
       292 <212> TYPE: DNA
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VERIFICATION SUMMARY　　　　　　　　DATE: 08/17/2001
PATENT APPLICATION:　US/09/852,238　　TIME: 11:40:04

Input Set : A:\51320-AB.txt
Output Set: N:\CRF3\08162001\I852238.raw

```
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:21 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:21 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:28 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:30 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:30 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:37 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:39 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:39 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:46 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:48 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:48 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:104 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:106 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:106 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:113 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:115 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:115 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:122 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:124 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:124 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:131 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:133 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:133 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:140 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:142 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:142 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:149 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:151 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:151 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:158 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:160 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:160 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:167 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:169 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:169 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:176 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:178 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:178 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:185 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:187 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:187 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:194 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:196 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:196 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:205 M:258 W: Mandatory Feature missing, <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 08/17/2001
PATENT APPLICATION: US/09/852,238   TIME: 11:40:04

Input Set : A:\51320-AB.txt
Output Set: N:\CRF3\08162001\I852238.raw

```
L:205 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:212 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:214 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:214 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:221 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:223 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:223 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:230 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:232 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:232 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:239 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:241 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:241 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:248 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:250 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:250 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:257 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:259 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:259 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:266 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:268 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:268 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:275 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:277 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:277 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:284 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:286 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:286 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:293 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
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